REMARKS

Claim 13 has been amended to provide antecedent basis for a human genome. New Claims 21 and 22 have been added. Claim 20 has been cancelled without prejudice to pursing the claim in a divisional, continuation, or continuation-in-part application. Claims 13 and 21-22 remain pending in the application. The Applicants have carefully considered all of the Examiner's rejections, but respectfully submit that the claims are allowable for at least the following reasons.

Rejections under § 112 – Enablement

The Examiner maintained her rejection of Claim 13 under 35 U.S.C. § 112, ¶ 1 for lack of enablement. The Examiner reiterated her previous statements and additionally noted several questions including: 1) How does detecting differences in fingerprints tell one anything about a potential target? 2) Just because binding affinities are different does not indicate that the random proteins from the human genome and the proteins from the pathogen are in any way similar or could be potential targets. At what point would one of skill in the art know if the pathogen target is analogous to the human target? 3) There are several thousand proteins in the human genome. Are all of these analyzed?

In order to satisfy the enablement requirement, the disclosure in the specification must contain sufficient information such that one of skill in the art can make and use the claimed invention without undue experimentation. *E.g.*, M.P.E.P. § 2164.01. "A patent need not teach, and preferably omits, what is well known in the art." *Id.* "As long as the specification discloses at least one method for making and using the claimed invention that bears a reasonable correlation to the entire scope of the claim, then the enablement requirement of 35 U.S.C. 112 is satisfied." M.P.E.P. § 2164.01(b). "If a statement of utility in the specification contains within it a connotation of how to use, and/or the art recognizes that standard modes of administration are known or contemplated, 35 U.S.C. 112 is satisfied." M.P.E.P. § 2164.01(c). It is important to note that the claims do not need to teach how to make and use the invention; rather, it is the specification that either fulfills or does not fulfill the enablement requirement. The Applicants respectfully submit that the instant specification provides such a teaching.

Claim 13 is a method claim containing six steps. The specification teaches how to make and use each step as follows:

(a) selecting a first potential target protein in said biochemical pathway and expressed by a pathogen genome

The specification states:

> In one embodiment, a biochemical pathway is identified for intervention. As one example, a metabolic pathway in a disease pathogen may be selected which involves the activity of ten different proteins. If any of these ten proteins are inactivated, the biochemical chain will be broken and the pathogen will be killed.

Page 10, lines 4-7. Thus, the specification teaches one way of how to perform element (a). For example, the specification teaches in one embodiment to select a potential target protein by choosing a protein that is part of a biochemical chain in a pathogen necessary for the pathogen to survive. Those of skill in the art would know how to identify which proteins in various biochemical chains would cause a pathogen to die if they were effectively removed. In other words, those of skill in the art would be able to determine proteins that are ***potential*** target proteins (e.g., those that would cause adverse effects in a pathogen if successfully targeted). The discussion below with regard to the rest of the claim elements describes how to use the selected potential target protein.

(b) retrieving a first interaction fingerprint comprising a set of values representative of binding strength between said potential target protein expressed by said pathogen genome and a corresponding set of ligands

The specification states, "the collection of derived annotations, including ligand interaction annotations...are stored within the genomic proteomics database 20 for subsequent retrieval and analysis." Page 6, lines 16-18. Thus, the specification teaches one way of how to perform element (b). For example, the specification teaches in one embodiment that interaction fingerprints (e.g., ligand interaction annotations) may be retrieved from a database. Those of skill in the art would know how to make a database and a system to retrieve information from the database. The discussion below with regard to the rest of the claim elements describes how to use the first retrieved interaction fingerprint.

(c) retrieving a second interaction fingerprint comprising a set of values representative of binding strength between a protein expressed by a human genome and said set of ligands

As discussed above with respect to element (b), the specification teaches how to perform the step of retrieving an interaction fingerprint. The specification teaches to use the retrieved interaction fingerprints to determine the pathogen protein interaction fingerprint overlap with interaction fingerprints for human genome proteins. Specification, page 10, lines 7-9.

(d) detecting differences between said first interaction fingerprint and said second interaction fingerprint

The specification teaches one way of how to perform the detecting step by describing in detail how fingerprint overlaps may be determined. *See* specification, page 8, lines 5-23 and Figure 5. Specifically, the specification teaches vector multiplication of two vectors, each representing an interaction fingerprint of a protein. It is described how in one example, an interaction vector may include the value of 1 for each ligand that binds with a protein and a value of 0 for each ligand that does not bind. Alternatively, "numerical variables such as estimated binding constants are used instead of binary 1 and 0 values." Specification, page 8, lines 22-23. Vector multiplication to produce a scalar value (i.e., the "dot product" of two vectors) has been well known in the art for hundreds of years and is recognized to produce a value indicative of the amount of overlap (i.e., the amount of similarity) between the two vectors. Accordingly, the specification teaches one of skill in the art one way to detect differences between two interaction fingerprints.

The specification also teaches how to use the detected differences. The specification notes that fingerprint comparisons indicate whether two proteins are "structurally or functionally associated." Specification, page 7, lines 30-31. Specifically, the specification teaches that higher overlap values "indicate proteins with similar chemical response" while lower overlap values indication "divergent chemical response." Specification, page 8, lines 27-29. Accordingly, one of skill in the art would know that they could use differences between interaction fingerprints to determine whether two proteins would react similarly to the same compound.

(e) repeating steps (c) and (d) for a plurality of different proteins encoded by the human genome

As described above, the specification teaches how to perform the steps of retrieving interaction fingerprints and detecting differences between interaction fingerprints. Accordingly, the specification teaches how to perform the repeating step. The specification also teaches how

to use the repetition (i.e., how to use detected differences between the interaction fingerprint of a pathogen protein and multiple human proteins). In one example, the specification teaches to determine the interaction fingerprint overlap between a potential target protein in a pathogen with "each protein of the human genome." Specification, page 10, lines 8-9. The specification teaches in one example to look for target proteins that have low average overlap or low maximum overlap with human proteins. Specification, page 10, lines 9-17. Such low overlaps indicate that a drug that is effective against the pathogen protein is not likely to bind with the tested human proteins and thus to have a low incidence of undesired side effects. *Id.*

(f) identifying said potential target protein as a target protein for pharmaceutical intervention based at least in part on said detected differences

In one example, the specification teaches that a potential target protein in a pathogen may be "identified as the best candidate[] for pharmaceutical intervention" based on low average or low maximum overlap with human proteins because such low overlap indicates that a drug binding to the potential target protein will not likely bind to the human proteins. Specification, page 10, lines 13-17. Accordingly, the specification teaches one way to perform the identifying step.

As already discussed, the specification teaches that one use of such an identification is that a potential target protein (e.g., one that would adversely affect a pathogen if successfully targeted) is identified as a good "candidate of pharmaceutical intervention because a ligand which inactivates [the] pathogen protein[] is less likely to bind to human proteins with resulting undesired side effects." Specification, page 10, lines 15-17. In other words, what was a potential target protein is now identified as a target substrate for attempting to find a drug that is active against it. The benefit of the claimed invention is clear. Out of several possible potential target pathogen proteins (i.e. those that if targeted would lead to an efficacious result), specific target proteins may be identified that have a higher probability of forming a basis for successful pharmaceutical intervention.

As discussed in detail above, the Applicants respectfully submit that how to make and use each and every limitation of the claims is taught in the specification. In order to advance prosecution, if the Examiner still believes that enablement is not satisfied, the Applicants request that she identify which limitations she believes are not enabled and whether the specification fails to teach 1) how to make or 2) how to use the identified limitations.

Rejections under § 112 – Indefiniteness

The Examiner rejected Claim 13 under 35 U.S.C. § 112, ¶ 2 as being indefinite. The Examiner asserted that there was no antecedent basis for "the human genome." The Applicants have amended Claim 13 to introduce "a human genome," thereby rendering the Examiner's rejection moot.

CONCLUSION

The Applicant respectfully submits that by the foregoing amendments and remarks they have overcome the Examiner's rejections and request a timely issuance of a Notice of Allowance.

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

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